

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/523,362
Source: PG7/10
Date Processed by STIC: 2/22/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/22/2005

PATENT APPLICATION: US/10/523,362

TIME: 08:54:20

Input Set : A:\532622010300.txt

Output Set: N:\CRF4\02222005\J523362.raw

4 <110> APPLICANT: Chardonnens, Agnes
5 Puzio, Piotr
7 <120> TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with
Abiotic Stress Response
8
10 <130> FILE REFERENCE: 532622010300
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/523,362
13 <141> CURRENT FILING DATE: 2005-02-07
15 <160> NUMBER OF SEQ ID NOS: 55
16 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 333
21 <212> TYPE: DNA
22 <213> ORGANISM: Saccharomyces cerevisiae
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(330)
26 <223> OTHER INFORMATION: GRX1
28 <400> SEQUENCE: 1
29 atg gta tct caa gaa act atc aag cac gtc aag gac ctt att gca gaa 48
30 Met Val Ser Gln Glu Thr Ile Lys His Val Lys Asp Leu Ile Ala Glu
31 1 5 10 15
33 aac gag atc ttc gtc gca tcc aaa acg tac tgt cca tac tgc cat gca 96
34 Asn Glu Ile Phe Val Ala Ser Lys Thr Tyr Cys Pro Tyr Cys His Ala
35 20 25 30
37 gcc cta aac acg ctt ttt gaa aag tta aag gtt ccc agg tcc aaa gtt 144
38 Ala Leu Asn Thr Leu Phe Glu Lys Leu Lys Val Pro Arg Ser Lys Val
39 35 40 45
41 ctg gtt ttg caa ttg aat gac atg aag gaa ggc gca gac att cag gct 192
42 Leu Val Leu Gln Leu Asn Asp Met Lys Glu Gly Ala Asp Ile Gln Ala
43 50 55 60
45 gcg tta tat gag att aat ggc caa aga acc gtg cca aac atc tat att 240
46 Ala Leu Tyr Glu Ile Asn Gly Gln Arg Thr Val Pro Asn Ile Tyr Ile
47 65 70 75 80
49 aat ggt aaa cat att gga ggc aac gac gac ttg cag gaa ttg agg gag 288
50 Asn Gly Lys His Ile Gly Gly Asn Asp Asp Leu Gln Glu Leu Arg Glu
51 85 90 95
53 act ggt gaa ttg gag gaa ttg tta gaa cct att ctt gca aat taa 333
54 Thr Gly Glu Leu Glu Glu Leu Leu Glu Pro Ile Leu Ala Asn
55 100 105 110
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 110
60 <212> TYPE: PRT
61 <213> ORGANISM: Saccharomyces cerevisiae

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62 <400> SEQUENCE: 2

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64 Met Val Ser Gln Glu Thr Ile Lys His Val Lys Asp Leu Ile Ala Glu
65 1          5          10          15
68 Asn Glu Ile Phe Val Ala Ser Lys Thr Tyr Cys Pro Tyr Cys His Ala
69          20          25          30
72 Ala Leu Asn Thr Leu Phe Glu Lys Leu Lys Val Pro Arg Ser Lys Val
73          35          40          45
76 Leu Val Leu Gln Leu Asn Asp Met Lys Glu Gly Ala Asp Ile Gln Ala
77          50          55          60
80 Ala Leu Tyr Glu Ile Asn Gly Gln Arg Thr Val Pro Asn Ile Tyr Ile
81 65          70          75          80
84 Asn Gly Lys His Ile Gly Gly Asn Asp Asp Leu Gln Glu Leu Arg Glu
85          85          90          95
88 Thr Gly Glu Leu Glu Glu Leu Leu Glu Pro Ile Leu Ala Asn
89          100          105          110

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92 <210> SEQ ID NO: 3

93 <211> LENGTH: 432

94 <212> TYPE: DNA

95 <213> ORGANISM: *Saccharomyces cerevisiae*

96 <220> FEATURE:

97 <221> NAME/KEY: CDS

98 <222> LOCATION: (1)..(432)

99 <223> OTHER INFORMATION:

W--> 101 <400> 3

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102 atg gag acc aat ttt tcc ttc gac tcg aat tta att gtt att atc att      48
103 Met Glu Thr Asn Phe Ser Phe Asp Ser Asn Leu Ile Val Ile Ile Ile
104 1          5          10          15
106 atc acg ttg ttt gcc aca aga att att gct aaa aga ttt tta tct act      96
107 Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
108          20          25          30
110 cca aaa atg gta tcc cag gaa aca gtt gct cac gta aag gat ctg att      144
111 Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
112          35          40          45
114 ggc caa aag gaa gtg ttt gtt gca gca aag aca tac tgc cct tac tgt      192
115 Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
116          50          55          60
118 aaa gct act ttg tct acc ctc ttc caa gaa ttg aac gtt ccc aaa tcc      240
119 Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
120 65          70          75          80
122 aag gcc ctt gtg ttg gaa tta gat gaa atg agc aat ggc tca gag att      288
123 Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
124          85          90          95
126 caa gac gct tta gaa gaa atc tcg ggc caa aaa act gta cct aac gta      336
127 Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
128          100          105          110
130 tac atc aat ggc aag cac att ggt ggt aac agc gat ttg gaa act ttg      384
131 Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
132          115          120          125
134 aag aaa aat ggc aag tta gct gaa ata ttg aag ccg gta ttt caa tag      432

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135 Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
136      130      135      140
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 143
141 <212> TYPE: PRT
142 <213> ORGANISM: Saccharomyces cerevisiae
143 <400> SEQUENCE: 4
145 Met Glu Thr Asn Phe Ser Phe Asp Ser Asn Leu Ile Val Ile Ile Ile
146 1      5      10      15
149 Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
150      20      25      30
153 Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
154      35      40      45
157 Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
158      50      55      60
161 Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
162 65      70      75      80
165 Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
166      85      90      95
169 Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
170      100     105     110
173 Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
174      115     120     125
177 Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
178      130     135     140
181 <210> SEQ ID NO: 5
182 <211> LENGTH: 858
183 <212> TYPE: DNA
184 <213> ORGANISM: Saccharomyces cerevisiae
185 <220> FEATURE:
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (1)..(855)
188 <223> OTHER INFORMATION: GRX3
190 <400> SEQUENCE: 5
191 atg tgt tct ttt cag gtt cca tct gca ttt tct ttt aac tac acc tcg      48
192 Met Cys Ser Phe Gln Val Pro Ser Ala Phe Ser Phe Asn Tyr Thr Ser
193 1      5      10      15
195 tac tgt tat aaa cgc cac caa gca aga tat tac aca gca gca aaa ctt      96
196 Tyr Cys Tyr Lys Arg His Gln Ala Arg Tyr Tyr Thr Ala Ala Lys Leu
197      20      25      30
199 ttt cag gaa atg cct gtt att gaa att aac gat caa gag caa ttt act      144
200 Phe Gln Glu Met Pro Val Ile Glu Ile Asn Asp Gln Glu Gln Phe Thr
201      35      40      45
203 tac cta act acc act gcg gcc ggc gac aag tta atc gtg ctt tat ttc      192
204 Tyr Leu Thr Thr Thr Ala Ala Gly Asp Lys Leu Ile Val Leu Tyr Phe
205      50      55      60
207 cat acc agt tgg gca gaa cca tgc aaa gca tta aag cag gtt ttt gag      240
208 His Thr Ser Trp Ala Glu Pro Cys Lys Ala Leu Lys Gln Val Phe Glu
209 65      70      75      80

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211 gcc att agt aat gag cct tcc aat tcc aac gtc tct ttc tta tcc att      288
212 Ala Ile Ser Asn Glu Pro Ser Asn Ser Asn Val Ser Phe Leu Ser Ile
213      85      90      95
215 gat gcg gac gaa aac tcg gaa att tca gaa ctt ttt gaa atc tca gct      336
216 Asp Ala Asp Glu Asn Ser Glu Ile Ser Glu Leu Phe Glu Ile Ser Ala
217      100      105      110
219 gtt cca tat ttt atc ata att cac aaa ggg aca atc tta aaa gaa tta      384
220 Val Pro Tyr Phe Ile Ile Ile His Lys Gly Thr Ile Leu Lys Glu Leu
221      115      120      125
223 tcc ggc gcg gat cca aag gag tat gtg tct tta tta gaa gac tgc aag      432
224 Ser Gly Ala Asp Pro Lys Glu Tyr Val Ser Leu Leu Glu Asp Cys Lys
225      130      135      140
227 aac tca gtc aat tcc gga tca tca caa act cat act atg gaa aat gca      480
228 Asn Ser Val Asn Ser Gly Ser Ser Gln Thr His Thr Met Glu Asn Ala
229 145      150      155      160
231 aac gta aat gag ggg agt cat aat gat gaa gac gat gac gac gaa gaa      528
232 Asn Val Asn Glu Gly Ser His Asn Asp Glu Asp Asp Asp Asp Glu Glu
233      165      170      175
235 gag gaa gaa gaa act gag gag caa ata aac gct aga ttg act aaa ttg      576
236 Glu Glu Glu Glu Thr Glu Glu Gln Ile Asn Ala Arg Leu Thr Lys Leu
237      180      185      190
239 gtc aat gcc gcg ccg gta atg tta ttt atg aag ggg agc ccc tct gaa      624
240 Val Asn Ala Ala Pro Val Met Leu Phe Met Lys Gly Ser Pro Ser Glu
241      195      200      205
243 cct aaa tgc ggg ttt tcg aga caa ctt gtg ggt atc ttg aga gaa cat      672
244 Pro Lys Cys Gly Phe Ser Arg Gln Leu Val Gly Ile Leu Arg Glu His
245      210      215      220
247 caa gta aga ttt ggc ttc ttt gat ata tta aga gac gaa tct gtt aga      720
248 Gln Val Arg Phe Gly Phe Phe Asp Ile Leu Arg Asp Glu Ser Val Arg
249 225      230      235      240
251 caa aac ttg aaa aag ttt tct gaa tgg cca act ttc cct caa ctt tat      768
252 Gln Asn Leu Lys Lys Phe Ser Glu Trp Pro Thr Phe Pro Gln Leu Tyr
253      245      250      255
255 ata aat ggg gag ttt caa ggc ggt tta gac att atc aag gaa tcc ttg      816
256 Ile Asn Gly Glu Phe Gln Gly Gly Leu Asp Ile Ile Lys Glu Ser Leu
257      260      265      270
259 gag gaa gac cct gat ttt ttg cag cat gct ctc caa tct taa      858
260 Glu Glu Asp Pro Asp Phe Leu Gln His Ala Leu Gln Ser
261      275      280      285
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 285
266 <212> TYPE: PRT
267 <213> ORGANISM: Saccharomyces cerevisiae
268 <400> SEQUENCE: 6
270 Met Cys Ser Phe Gln Val Pro Ser Ala Phe Ser Phe Asn Tyr Thr Ser
271 1      5      10      15
274 Tyr Cys Tyr Lys Arg His Gln Ala Arg Tyr Tyr Thr Ala Ala Lys Leu
275      20      25      30
278 Phe Gln Glu Met Pro Val Ile Glu Ile Asn Asp Gln Glu Gln Phe Thr

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279          35          40          45
282 Tyr Leu Thr Thr Thr Ala Ala Gly Asp Lys Leu Ile Val Leu Tyr Phe
283          50          55          60
286 His Thr Ser Trp Ala Glu Pro Cys Lys Ala Leu Lys Gln Val Phe Glu
287 65          70          75          80
290 Ala Ile Ser Asn Glu Pro Ser Asn Ser Asn Val Ser Phe Leu Ser Ile
291          85          90          95
294 Asp Ala Asp Glu Asn Ser Glu Ile Ser Glu Leu Phe Glu Ile Ser Ala
295          100          105          110
298 Val Pro Tyr Phe Ile Ile Ile His Lys Gly Thr Ile Leu Lys Glu Leu
299          115          120          125
302 Ser Gly Ala Asp Pro Lys Glu Tyr Val Ser Leu Leu Glu Asp Cys Lys
303          130          135          140
306 Asn Ser Val Asn Ser Gly Ser Ser Gln Thr His Thr Met Glu Asn Ala
307 145          150          155          160
310 Asn Val Asn Glu Gly Ser His Asn Asp Glu Asp Asp Asp Asp Glu Glu
311          165          170          175
314 Glu Glu Glu Glu Thr Glu Glu Gln Ile Asn Ala Arg Leu Thr Lys Leu
315          180          185          190
318 Val Asn Ala Ala Pro Val Met Leu Phe Met Lys Gly Ser Pro Ser Glu
319          195          200          205
322 Pro Lys Cys Gly Phe Ser Arg Gln Leu Val Gly Ile Leu Arg Glu His
323          210          215          220
326 Gln Val Arg Phe Gly Phe Phe Asp Ile Leu Arg Asp Glu Ser Val Arg
327 225          230          235          240
330 Gln Asn Leu Lys Lys Phe Ser Glu Trp Pro Thr Phe Pro Gln Leu Tyr
331          245          250          255
334 Ile Asn Gly Glu Phe Gln Gly Gly Leu Asp Ile Ile Lys Glu Ser Leu
335          260          265          270
338 Glu Glu Asp Pro Asp Phe Leu Gln His Ala Leu Gln Ser
339          275          280          285
342 <210> SEQ ID NO: 7
343 <211> LENGTH: 735
344 <212> TYPE: DNA
345 <213> ORGANISM: Saccharomyces cerevisiae
346 <220> FEATURE:
347 <221> NAME/KEY: CDS
348 <222> LOCATION: (1)..(732)
349 <223> OTHER INFORMATION: GRX4
351 <400> SEQUENCE: 7
352 atg act gtg gtt gaa ata aaa agc cag gac caa ttt acg caa cta acc      48
353 Met Thr Val Val Glu Ile Lys Ser Gln Asp Gln Phe Thr Gln Leu Thr
354 1          5          10          15
356 act aca aac gct gct aat aaa ctc att gtc tta tat ttt aaa gct caa      96
357 Thr Thr Asn Ala Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
358          20          25          30
360 tgg gct gat cct tgc aaa act atg agc cag gtg cta gaa gct gtt agt      144
361 Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
362          35          40          45

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/523,362

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Input Set : A:\532622010300.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:51,52,53,54,55

VERIFICATION SUMMARYPATENT APPLICATION: **US/10/523,362**

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Input Set : **A:\532622010300.txt**Output Set: **N:\CRF4\02222005\J523362.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:99
L:2765 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51
L:2779 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:52
L:2793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:53
L:2807 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54
L:2821 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:55